

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: Ryan

Serial No.: 10/608,463

Group Art Unit: 1652

Filed: June 27, 2003

Examiner: T. Saidha

FOR: ISOLATED GENOMIC POLYNUCLEOTIDE FRAGMENTS FROM  
CHROMOSOME 12 THAT ENCODE HUMAN CARBOXYPEPTIDASE M AND THE  
HUMAN MOUSE DOUBLE MINUTE 2 HOMOLOG

Confirmation No.: 6428

**RESPONSE TO NOTIFICATION OF NONCOMPLIANT APPEAL BRIEF**

Mail Stop Appeal  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

This is in response to the Response to Notification of Noncompliant Appeal Brief  
dated October 26, 2009.

## **R E M A R K S**

In the Notification of Non-Compliant Appeal Brief, it was stated:

The summary of claimed subject matter identify the independent claim 1, instead of claim 7, which is a typographical error. In the claims appendix withdrawn claims 22, 23 and 32 are mentioned, please remove. An entire brief is no required just the defective sections may be submitted.

In response, Appellant herewith submits pages 3-12 of the Appeal Brief containing the corrected Summary of Claimed Subject Matter and a Claims Appendix where withdrawn claims 22, 23 and 32 have been removed.

In view of this response, Appellant asserts that this Appeal is in condition for further consideration. The Examiner is invited to contact the undersigned at (914) 712-0093 if there are further questions regarding this application or appeal.

Respectfully submitted,

Date: November 26, 2009

/Cheryl H Agris/

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Customer No. 25538

## **I. REAL PARTY IN INTEREST**

The real party in interest of the present application is Ryogen LLC. Ryogen LLC is the owner of the present application by way of an assignment from the inventor, James W. Ryan of all rights, title, and interest.

## **II. RELATED APPEALS AND INTERFERENCES**

There are no appeals or interferences related to the present application.

## **III. STATUS OF CLAIMS**

Claims 7, 10, 15-18, 20, 24, 25, 30 and 31 stand finally rejected by the Examiner as noted in the Office Action mailed on January 2, 2009 and in the Advisory Action mailed June 24, 2009. Claims 1-6, 8-9, 11, 13, 19, 21 and 26-29 have been canceled. Claims 12, 14, 22, 23 and 32-38 have been withdrawn. The rejection of claims 7, 10, 15-18, 20, 24, 25, 30 and 31 is appealed.

## **IV. STATUS OF AMENDMENTS**

Amendments to claims 7 and 24 subsequent to the Examiner's Final Rejection mailed January 2, 2009 were submitted but were not entered.

## **V. SUMMARY OF THE CLAIMED SUBJECT MATTER**

### **A. Independent Claim 7**

Claim Elements	Support in specification
An isolated nucleic acid molecule 20-51039 contiguous nucleotides in length consisting of a reverse or forward strand of a region of SEQ ID NO:4	Page 9, line 34; page 10, lines 22-26
wherein said region is selected from the group consisting of a 5'-non coding region depicted in nucleotides 51039-41739 of SEQ ID NO:4, a 3'-non-coding region depicted in nucleotides 9503-1 of SEQ ID NO:4, a contiguous intron-exon region between nucleotides 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, a	Page 10: Table 2

contiguous exon-intron region between nucleotide 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, an intron depicted in nucleotides 36385-40645, 36309-33127, 32994-29616, 29564-25577, 25507-25384, 25287-21169, 21006-14110, 13953-13267, and/or 13188-10665, a region comprising a dinucleotide of the following group: 41739-41738, 40645-40646, 36309-36310, 36384-36385, 32994-32995, 33126-33127, 29564-29565, 29615-29616, 25507-25508, 25287-25288, 25383-25384, 25576-25577, 21006-21007, 21168-21169, 14109-14110, 13953-13954, 13266-13267, 13188-13189, 10664-10665 and/or 9504-9503		
a transcription binding site selected from the group consisting of		Page 9, line 29 to page 10, line 2; Table 3 on pages 10-12
BINDING SITES	huMDM2, location in SEQ ID NO:4	
AP1_C:	36-46, 2876-2886;	
AP4_Q5:	7944-7980;	
AP4_Q6:	7943-59, 8924-8940, 9294-9310;	
ARNT_01:	1682-1706, 2193-2217, 9201-9225;	
BRN2_01:	1040-1058, 7803-7821;	
CAAT_01:	3292-3306;	
CDPCR3HD_01:	6522-6540;	
CEBPB_01:	1424-1438, 3917-3931, 4178-4192, 4787-4801, 6855-6869;	
CREL_01:	5630-5642;	
DELTAEF1_01:	83-95, 6328-6340;	
FREAC7_01:	2757-2773, 5154-5170, 5823-5839;	
GATA1_04:	4846-4858, 7017-7029;	
GATA1_05:	8464-8476;	
GATA2_02:	6045-6057, 6073-6085, 6142-6154;	
GATA2_03:	2489-2501, 3323-3335, 3384-3396,	

7393-7405:	
GATA3_02:	3264-3276, 6870-6882;
GATA3_03:	40-52, 5729-5741, 6529-6541, 6874-6886, 7041-7053, 7589-7601;
GATA_C: 7	349-7361, 8188-8200;
HFH2_01:	1743-1759, 7995-8011;
HFH3_01:	502-518, 1739-1755, 4160-4176, 9402-9418, 9418-9434;
HFH8_01:	8184-8200;
IK2_01:	951-963, 3588-3600;
MZF1_01:	1202-1210, 1447-1455, 4997-4005, 5424-5432;
NF1_Q6:	1480-1500, 8166-8182;
NFAT_Q6:	4190-4208, 6009-6027;
NKX25_01:	741-755, 1648-1662, 1885-1899, 1984-1998, 3609-3623, 4928-4942, 5060-5074, 5889-5903, 8850-8864, 9190-9204;
NKX25_02:	2584-2599, 2970-2984, 4644-4658, 5179-5193, 6482-6496;
NMYC_01:	2560-2572;
RORA1_01:	220-238, 2638-2656;
S8_01:	4644-4656, 4842-4854, 4845-4857, 5200-5212, 5371-5383, 5735-5747, 6482-6494, 6541-6553, 6544-6556, 6772-6784, 7270-7292, 7273-7285;
SOX5_01:	1355-1371, 1430-1446, 3094-3110, 3155-3171, 4669-4685, 4692-4708, 4789-4805;
SRY_02:	4164-4180, 5665-5681;
TATA_01:	1261-1277, 2574-2590, 2723-2739, 2733-

2749, 2770-2786, 4199-4215, 4206-4222;	
TATA_C:	5900-5916, 7456-7472, 7702-7718, 7917-7933; and
XFD2_01:	7702-7218, 7917-7933;
a transcription binding site selected from the group consisting of	
BINDING SITES	huMDM2, location in SEQ ID NO:4
AP1_C:	12109-12119, 12695-12705, 22600-22610, 24166-24176, 31311-31321, 35234-35244, 39184-39194;
AP1_Q2:	11952-11962, 12068-12078, 14798-14808, 21748-21758, 22613-22623, 23676-23686, 26562-26572, 30046-30056;
AP1_Q4:	12695-12705, 31311-31321, 35234-35244, 36295-36305, 38784-38794, 39188-39198;
AP4_Q6:	31635-31651;
BRN2_01:	13448-13466, 14764-14782, 28094-28112, 40027-40045;
CAAT_01:	11288-11302, 15054-15068;
CDPCR3HD_01:	11286-11304, 13284-13302, 20846-20864, 29344-29362;
CEBPB_01:	29241-29255;
CREL_01:	36091-36103, 38873-38885;
DELTAEF1_01:	18083-18095, 20385-20397, 26955-26967;
FREAC7_01:	11982-11998, 15187-15202, 16523-16539, 16529-16545, 16587-16603, 16604-16620, 16676-16642, 16633-16649, 16644-16660, 16650-16666, 16657-16673, 16673-16689, 16762-16778, 21332-21348, 25689-25700, 26529-26545, 27767-27783, 29495-29511;
GATA1_02:	10916-10928, 15775-15789, 18162-18174, 26088-26100, 32518-32530;
GATA1_03:	28012-28024;

<p>GATA1_04: 11153-11165, 11630-11642, 13778-13790, 17439-17451, 19300-19312, 21606-21618, 22743-22755, 23747-23759, 25806-25818, 26529-26541, 29424-29436, 30455-30467, 32761-32778, 33352-33364, 33960-33972, 36101-36113, 40007-40019;</p> <p>GATA1_05: 11590-11602, 26550-26562, 36737-36749;</p> <p>GATA1_06: 18772-18784, 23054-23066, 35568-35580, 37855-37867;</p> <p>GATA2_02: 20755-20767, 30830-30842, 34755-34767, 36285-36297, 39143-39155, 39641-39653, 40586-40598;</p> <p>GATA2_03: 13535-13547, 22711-22723, 23161-23173, 25028-25040, 27237-27249, 36277-36289;</p> <p>GATA3_02: 11558-11570, 16470-16482, 17225-17237, 19619-19631, 22156-22168, 22443-22455, 24713-24725, 27619-27631, 32716-32728, 34124-34136, 34163-34175, 36832-36844, 38403-38415;</p> <p>GATA3_03: 10869-10881, 11515-11527, 13845-13857, 17221-17233, 18952-18964, 20050-20062, 40171-40183;</p> <p>GATA_C: 15848-15860, 18899-18911, 23640-23652, 29072-29084, 30881-30893, 33198-33210, 37472-37484, 38621-38633;</p> <p>GFI1_01: 35469-35481, 35492-35504;</p> <p>HFH2_01: 15939-15955, 24636-24652, 25866-25882, 32171-32187, 35372-35388, 39457-35473;</p> <p>HFH3_01: 13340-13356, 19218-19234, 21328-21344, 21336-21352, 21344-21360, 28062-28078, 32125-32141;</p> <p>HFH8_01: 14133-14149, 22578-22584;</p> <p>HNF3B_01: 13150-13166, 16505-16521, 25264-25280, 29443-29459, 37654-37670;</p> <p>IK2_01: 11547-11559, 17144-17156, 18961-18973, 23883-23895, 27617-27629, 28908-28920, 29241-29253, 30752-30764, 34768-34780;</p>	
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LYF1_01:	12319-12331, 19191-19203, 37226-37238, 39430-39442;
MAX_01:	22974-22986, 33339-33351;
MZF1_01:	26105-26113, 35187-35195;
NF1_Q6:	12048-12064, 33334-33354;
NFAT_Q6:	13295-13313, 14157-14175, 14311-14329, 14414-14432, 18269-18287, 19326-19344, 20801-20819, 21177-21195, 22537-22555, 23861-23879, 25392-25410, 25879-25897, 27524-27542, 30636-30654, 30718-30736, 31525-31543, 33655-33673, 34726-34744, 34917-34535, 34990-35008, 35979-35997, 36479-36493, 36577-36595, 37154-37172, 40224-40242, 40365-40383;
NKX25_01:	12041-12055, 12340-12354, 12471-12485, 12742-12756, 12877-12891, 13849-13863, 18995-19009, 21440-21454, 21883-21897, 28426-28440, 30964-30978, 32033-32047, 32265-32279;
NKX25_02:	10998-11012, 12711-12725, 14131-14145, 14726-14740, 16024-16038;
NMYC_01:	18753-18765, 18754-18766, 23076-23088, 30534-30546, 34400-34412;
RORA1_01:	13134-13152, 22966-22984, 24934-24952, 33341-33359, 34760-34778;
S8_01:	11000-11012, 11977-11989, 12048-12060, 12051-12063, 13747-13759, 13923-13935, 13926-13938, 14676-14688, 14679-14691, 16026-16038, 16313-16325, 16316-16328, 17515-17527, 20756-20768, 20759-20771, 23154-23166, 23157-23169, 25198-25210, 25201-25213, 26651-26663, 27508-27520, 27511-27523, 29450-29462, 29478-28490, 29775-29787, 29778-29790, 29813-29825, 29816-29828, 31329-31341, 31677-31689, 31680-31692, 31732-31744, 31735-31747, 36137-36149, 36140-36152, 36812-36824, 36815-36827, 37413-37425, 38679-38691, 39474-39486, 39477-39489;
SOX5_01:	27397-27413, 27572-27588, 28100-28116, 29230-29246, 29439-29455, 30690-30706, 31595-31611, 33871-33887, 34113-34129, 34624-34640, 37668-37684, 38582-38598, 39124-



<p>39140, 40410-40426;</p> <p>SRY_02: 20016-20032, 22410-22426, 27329-27345, 29162-29178, 29499-29515, 30646-30662, 31503-31519, 35928-35944, 37324-37340;</p> <p>TATA_01: 32722-32738, 32729-32745, 32807-32823, 33825-33841, 34120-34136, 35433-35449, 36593-36609;</p> <p>TATA_C: 11015-11031, 11817-11833, 13635-13651, 14930-14946;</p> <p>TCF11_01: 18543-18549, 22574-22580, 31281-31297, 31489-31505, 38754-38770;</p> <p>USF_01: 23075-23087, 32577-32589;</p> <p>VMYB_02: 11526-11538, 17384-17396, 18400-18412, 19549-19561, 22188-22200, 40486-40508 and</p> <p>XFD2_01: 16620-16636. 18153-18169, 22102-22118, 23141-23157.</p> <p>And a transcription binding site selected from the group consisting of</p> <p>BINDING SITES huMDM2 location in SEQ ID NO:4</p> <p>AP1_C: 44584-44594, 49069-49079;</p> <p>AP1_Q2: 42174-42184, 45217-45227, 48422-48422, 50447-50457;</p> <p>AP1_Q4: 42702-42712, 50806-50816;</p> <p>AP4_Q6: 42117-42133, 42118-42134, 42244-42260, 45432-45448; 45433-45449, 46609-46625;</p> <p>BRN2_01: 42310-42328, 44022-44040, 47514-47532, 48900-48918, 48967-48985;</p> <p>CAAT_01: 44866-44880;</p> <p>CDPCR3HD_01: 45671-45689, 49219-49237;</p>	
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CREL_01:	42437-42449, 49797-49809;	
FREAC7_01:	47026-47042, 47292-47308, 47658-47674;	
GATA1_02:	43482-43494, 48926-48938, 49284-49296;	
GATA1_03:	47371-47383;	
GATA1_04:	43054-43066, 43162-43162, 43967-43979, 45464-45476, 45916-45928, 47763-47775;	
GATA1_05:	49319-49331, 49459-49471;	
GATA1_06:	47590-47602;	
GATA2_02:	42660-42672, 43475-43487;	
GATA2_03:	43714-43726, 50948-50960;	
GATA3_02:	49155-49167, 49844-49856;	
GATA3_03:	42202-42214, 44810-44822, 48438-48450, 49136-49148, 49337-49349, 49869-49881;	
GATA_C:	44011-44023, 45256-45268, 45823-45835, 47915-47927, 49201-49213, 49573-49585;	
GFI1_01:	46606-46618, 47063-47075;	
HFH3_01:	47030-47046, 47284-47300, 47288-47304;	
IK2_01:	45275-45287;	
LYF1_01:	44564-44576, 46991-47003, 49567-49579;	
MAX_01:	43234-43246, 48726-48738;	
MZF1_01:	41772-41780, 42290-42298, 42295-42303, 44507-44515, 45105-45113, 45203-45211, 49948-49956, 50774-50782;	
NF1_Q6:	50209-50229;	
NFAT_Q6:	42061-42079, 44418-44436, 46399-46417,	

47974-47992, 49267-49285, 49964-49982, 50392-50410;	
NKX25_01: 42394-42408, 43507-43521, 46115-46129;	
RORA1_01: 45073-45091, 48718-48736;	
S8_01: 43552-43564, 45214-45226, 47160-47172, 48419-48431, 49295-49307, 50379-50391;	
SOX5_01: 43716-43732, 46351-46367, 47156-47172, 47774-47790, 47868-47884, 47974-47990, 48915-48931, 50323-50339;	
TATA_01: 45588-45604, 47625-47641, 48026-48042, 48659-48675, 49056-49072, 49079-49095, 49152-49168;	
TCF11_01: 49115-49131;	
VMYB_02: 42010-42022, 42279-42291, 44651-44663;	a
XFD2_01: 42870-42886, 42910-42926.	

## B. Independent Claim 24

Claim Element	Support in Specification
An isolated nucleic acid molecule 20-5000 contiguous nucleotides in length	Page 9, line 35 to page 10, line 2
consisting of a reverse or forward strand of a contiguous exon intron region between nucleotides 41738-9502 of SEQ ID NO:4 or contiguous intron-exon region between nucleotides 41738-9502 of SEQ ID NO:4,	Page 10, Table 2 and page 14, lines 29-32
wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2	Page 2, lines 7-13; page 10, Table 2

## VI. GROUNDS OF REJECTION TO BE REVIEWED ON APPEAL

- A. Whether claims 7, 10, 15-18, 20, 24, 25, 30 and 31 comply with the written description requirement under 35 USC §112, first paragraph
- B. Whether claim 7, 10, 15-18, 20, 24, 25, 30 and 31 are unpatentable over Muzny et al. , Genbank Accession No. AC025423 (“Muzny”) in view of Vogelstein et al., US Patent No. 5,411,860 (“Vogelstein”).

## VII. ARGUMENT

### A. Claims 7, 10, 15-18, 20, 24, 25, 30 and 31 Comply With the Written Description Requirement

In the final rejection dated January 2, 2009, it was asserted that claim 7, with dependent claims 10, 15-18, 20, 30 and 31, as amended on March 3, 2005 and August 29, 2005 and claim 24, with dependent claim 25, added on March 3, 2005 and amended on August 29, 2005 to recite "wherein a sequence segment comprising 41738-9502 of SEQ ID NO: 4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, ... a region comprising a dinucleotide of the following group: 41739-41738, ..... and/or 9504-9503" (lines 12-15 of claim 7) constitutes new matter and lacks support. Appellant had traversed and pointed out that there is more than adequate support in the specification for claims 7, 10, 15-18, 20, 30 and 31 and in particular, for the sequence segment 41738-9502, the **nucleotide ranges** for the various sites for huMDM2 location in SEQ ID NO:4, specific ranges that relate to the specific dinucleotide ranges or specific ‘exon/intron’ organization in terms of the

## CLAIMS APPENDIX

7. An isolated nucleic acid molecule 20-51039 contiguous nucleotides in length consisting of a reverse or forward strand of a region of SEQ ID NO:4, wherein said region is selected from the group consisting of a 5'-non coding region depicted in nucleotides 51039-41739 of SEQ ID NO:4, a 3'-non-coding region depicted in nucleotides 9503-1 of SEQ ID NO:4, a contiguous intron-exon region between nucleotides 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, a contiguous exon-intron region between nucleotide 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2, an intron depicted in nucleotides 36385-40645, 36309-33127, 32994-29616, 29564-25577, 25507-25384, 25287-21169, 21006-14110, 13953-13267, and/or 13188-10665, a region comprising a dinucleotide of the following group: 41739-41738, 40645-40646, 36309-36310, 36384-36385, 32994-32995, 33126-33127, 29564-29565, 29615-29616, 25507-25508, 25287-25288, 25383-25384, 25576-25577, 21006-21007, 21168-21169, 14109-14110, 13953-13954, 13266-13267, 13188-13189, 10664-10665 and/or 9504-9503; a transcription binding site selected from the group consisting of

BINDING SITES	huMDM2, location in SEQ ID NO:4
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AP1_C:	36-46, 2876-2886;
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AP4_Q5:	7944-7980;
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AP4_Q6:	7943-59, 8924-8940, 9294-9310;
ARNT_01:	1682-1706, 2193-2217, 9201-9225;
BRN2_01:	1040-1058, 7803-7821;
CAAT_01:	3292-3306;
CDPCR3HD_01:	6522-6540;
CEBPB_01:	1424-1438, 3917-3931, 4178-4192, 4787-4801, 6855-6869;
CREL_01:	5630-5642;
DELTAEF1_01:	83-95, 6328-6340;
FREAC7_01:	2757-2773, 5154-5170, 5823-5839;
GATA1_04:	4846-4858, 7017-7029;
GATA1_05:	8464-8476;
GATA2_02:	6045-6057, 6073-6085, 6142-6154;
GATA2_03:	2489-2501, 3323-3335, 3384-3396, 7393-7405;

GATA3_02:	3264-3276, 6870-6882;
GATA3_03:	40-52, 5729-5741, 6529-6541, 6874-6886, 7041-7053, 7589-7601;
GATA_C: 7	349-7361, 8188-8200;
HFH2_01:	1743-1759, 7995-8011;
HFH3_01:	502-518, 1739-1755, 4160-4176, 9402-9418, 9418-9434;
HFH8_01:	8184-8200;
IK2_01:	951-963, 3588-3600;
MZF1_01:	1202-1210, 1447-1455, 4997-4005, 5424-5432;
NF1_Q6:	1480-1500, 8166-8182;
NFAT_Q6:	4190-4208, 6009-6027;
NKX25_01:	741-755, 1648-1662, 1885-1899, 1984-1998, 3609-3623, 4928-4942, 5060-5074, 5889-5903, 8850-8864, 9190-9204;
NKX25_02:	2584-2599, 2970-2984, 4644-4658, 5179-5193, 6482-6496;

NMYC\_01: 2560-2572;

RORA1\_01: 220-238, 2638-2656;

S8\_01: 4644-4656, 4842-4854, 4845-4857, 5200-5212, 5371-5383, 5735-5747,  
6482-6494, 6541-6553, 6544-6556, 6772-6784, 7270-7292, 7273-7285;

SOX5\_01: 1355-1371, 1430-1446, 3094-3110, 3155-3171, 4669-4685, 4692-4708,  
4789-4805;

SRY\_02: 4164-4180, 5665-5681;

TATA\_01: 1261-1277, 2574-2590, 2723-2739, 2733-2749, 2770-2786, 4199-4215,  
4206-4222;

TATA\_C: 5900-5916, 7456-7472, 7702-7718, 7917-7933; and

XFD2\_01: 7702-7218, 7917-7933; .

a transcription binding site selected from the group consisting of

BINDING SITES huMDM2, location in SEQ ID NO:4

AP1\_C: 12109-12119, 12695-12705, 22600-22610, 24166-24176, 31311-31321, 35234-  
35244, 39184-39194;



AP1\_Q2: 11952-11962, 12068-12078, 14798-14808, 21748-21758, 22613-22623, 23676-23686, 26562-26572, 30046-30056;

AP1\_Q4: 12695-12705, 31311-31321, 35234-35244, 36295-36305, 38784-38794, 39188-39198;

AP4\_Q6: 31635-31651;

BRN2\_01: 13448-13466, 14764-14782, 28094-28112, 40027-40045;

CAAT\_01: 11288-11302, 15054-15068;

CDPCR3HD\_01: 11286-11304, 13284-13302, 20846-20864, 29344-29362;

CEBPB\_01: 29241-29255;

CREL\_01: 36091-36103, 38873-38885;

DELTAEF1\_01: 18083-18095, 20385-20397, 26955-26967;

FREAC7\_01: 11982-11998, 15187-15202, 16523-16539, 16529-16545, 16587-16603, 16604-16620, 16676-16642, 16633-16649, 16644-16660, 16650-16666, 16657-16673, 16673-16689, 16762-16778, 21332-21348, 25689-25700, 26529-26545, 27767-27783, 29495-29511;

GATA1\_02: 10916-10928, 15775-15789, 18162-18174, 26088-26100, 32518-32530;

GATA1\_03: 28012-28024;

GATA1\_04: 11153-11165, 11630-11642, 13778-13790, 17439-17451, 19300-19312, 21606-21618, 22743-22755, 23747-23759, 25806-25818, 26529-26541, 29424-29436, 30455-30467, 32761-32778, 33352-33364, 33960-33972, 36101-36113, 40007-40019;

GATA1\_05: 11590-11602, 26550-26562, 36737-36749;

GATA1\_06: 18772-18784, 23054-23066, 35568-35580, 37855-37867;

GATA2\_02: 20755-20767, 30830-30842, 34755-34767, 36285-36297, 39143-39155, 39641-39653, 40586-40598;

GATA2\_03: 13535-13547, 22711-22723, 23161-23173, 25028-25040, 27237-27249, 36277-36289;

GATA3\_02: 11558-11570, 16470-16482, 17225-17237, 19619- 19631, 22156-22168, 22443-22455, 24713-24725, 27619-27631, 32716-32728, 34124-34136, 34163-34175, 36832-36844, 38403-38415;

GATA3\_03: 10869-10881, 11515-11527, 13845-13857, 17221-17233, 18952-18964, 20050-20062, 40171-40183;

GATA\_C: 15848-15860, 18899-18911, 23640-23652, 29072-29084, 30881-30893, 33198-33210, 37472-37484, 38621-38633;

GFII\_01: 35469-35481, 35492-35504;

HFH2\_01: 15939-15955, 24636-24652, 25866-25882, 32171-32187, 35372-35388, 39457-35473;

HFH3\_01: 13340-13356, 19218-19234, 21328-21344, 21336-21352, 21344-21360, 28062-28078, 32125-32141;

HFH8\_01: 14133-14149, 22578-22584;

HNF3B\_01: 13150-13166, 16505-16521, 25264-25280, 29443-29459, 37654-37670;

IK2\_01: 11547-11559, 17144-17156, 18961-18973, 23883-23895, 27617-27629, 28908-28920, 29241-29253, 30752-30764, 34768-34780;

LYF1\_01: 12319-12331, 19191-19203, 37226-37238, 39430-39442;

MAX\_01: 22974-22986, 33339-33351;

MZF1\_01: 26105-26113, 35187-35195;

NF1\_Q6: 12048-12064, 33334-33354;

NFAT\_Q6: 13295-13313, 14157-14175, 14311-14329, 14414-14432, 18269-18287, 19326-19344, 20801-20819, 21177-21195, 22537-22555, 23861-23879, 25392-25410, 25879-25897, 27524-

27542, 30636-30654, 30718-30736, 31525-31543, 33655-33673, 34726-34744, 34917-34535, 34990-35008, 35979-35997, 36479-36493, 36577-36595, 37154-37172, 40224-40242, 40365-40383;

NKX25\_01: 12041-12055, 12340-12354, 12471-12485, 12742-12756, 12877-12891, 13849-13863, 18995-19009, 21440-21454, 21883-21897, 28426-28440, 30964-30978, 32033-32047, 32265-32279;

NKX25\_02: 10998-11012, 12711-12725, 14131-14145, 14726-14740, 16024-16038;

NMYC\_01: 18753-18765, 18754-18766, 23076-23088, 30534-30546, 34400-34412;

RORA1\_01: 13134-13152, 22966-22984, 24934-24952, 33341-33359, 34760-34778;

S8\_01: 11000-11012, 11977-11989, 12048-12060, 12051-12063, 13747-13759, 13923-13935, 13926-13938, 14676-14688, 14679-14691, 16026-16038, 16313-16325, 16316-16328, 17515-17527, 20756-20768, 20759-20771, 23154-23166, 23157-23169, 25198-25210, 25201-25213, 26651-26663, 27508-27520, 27511-27523, 29450-29462, 29478-28490, 29775-29787, 29778-29790, 29813-29825, 29816-29828, 31329-31341, 31677-31689, 31680-31692, 31732-31744, 31735-31747, 36137-36149, 36140-36152, 36812-36824, 36815-36827, 37413-37425, 38679-38691, 39474-39486, 39477-39489;

SOX5\_01: 27397-27413, 27572-27588, 28100-28116, 29230-29246, 29439-29455, 30690-30706, 31595-31611, 33871-33887, 34113-34129, 34624-34640, 37668-37684, 38582-38598, 39124-39140, 40410-40426;

SRY\_02: 20016-20032, 22410-22426, 27329-27345, 29162-29178, 29499-29515, 30646-

30662, 31503-31519, 35928-35944, 37324-37340;

TATA\_01: 32722-32738, 32729-32745, 32807-32823, 33825-33841, 34120-34136, 35433-35449, 36593-36609;

TATA\_C: 11015-11031, 11817-11833, 13635-13651, 14930-14946;

TCF11\_01: 18543-18549, 22574-22580, 31281-31297, 31489-31505, 38754-38770;

USF\_01: 23075-23087, 32577-32589;

VMYB\_02: 11526-11538, 17384-17396, 18400-18412, 19549-19561, 22188-22200, 40486-40508 and

XFD2\_01: 16620-16636, 18153-18169, 22102-22118, 23141-23157.

And a transcription binding site selected from the group consisting of

#### BINDING SITES

huMDM2, 1 location in SEQ ID NO:4

AP1\_C: 44584-44594, 49069-49079;

AP1\_Q2: 42174-42184, 45217-45227, 48422-48422, 50447-50457;

AP1_Q4:	42702-42712, 50806-50816;
AP4_Q6:	42117-42133, 42118-42134, 42244-42260, 45432-45448; 45433-45449, 46609-46625;
BRN2_01:	42310-42328, 44022-44040, 47514-47532, 48900-48918, 48967-48985;
CAAT_01:	44866-44880;
CDPCR3HD_01:	45671-45689, 49219-49237;
CREL_01:	42437-42449, 49797-49809;
FREAC7_01:	47026-47042, 47292-47308, 47658-47674;
GATA1_02:	43482-43494, 48926-48938, 49284-49296;
GATA1_03:	47371-47383;
GATA1_04:	43054-43066, 43162-43162, 43967-43979, 45464-45476, 45916-45928, 47763-47775;
GATA1_05:	49319-49331, 49459-49471;
GATA1_06:	47590-47602;

GATA2_02:	42660-42672, 43475-43487;
GATA2_03:	43714-43726, 50948-50960;
GATA3_02:	49155-49167, 49844-49856;
GATA3_03:	42202-42214, 44810-44822, 48438-48450, 49136-49148, 49337-49349, 49869-49881;
GATA_C:	44011-44023, 45256-45268, 45823-45835, 47915-47927, 49201-49213, 49573-49585;
GFI1_01:	46606-46618, 47063-47075;
HFH3_01:	47030-47046, 47284-47300, 47288-47304;
IK2_01:	45275-45287;
LYF1_01:	44564-44576, 46991-47003, 49567-49579;
MAX_01:	43234-43246, 48726-48738;
MZF1_01:	41772-41780, 42290-42298, 42295-42303, 44507-44515, 45105-45113, 45203-45211, 49948-49956, 50774-50782;

NF1_Q6:	50209-50229;
NFAT_Q6:	42061-42079, 44418-44436, 46399-46417, 47974-47992, 49267-49285, 49964-49982, 50392-50410;
NKX25_01:	42394-42408, 43507-43521, 46115-46129;
RORA1_01:	45073-45091, 48718-48736;
S8_01:	43552-43564, 45214-45226, 47160-47172, 48419-48431, 49295-49307, 50379-50391;
SOX5_01:	43716-43732, 46351-46367, 47156-47172, 47774-47790, 47868-47884, 47974-47990, 48915-48931, 50323-50339;
TATA_01:	45588-45604, 47625-47641, 48026-48042, 48659-48675, 49056-49072, 49079-49095, 49152-49168;
TCF11_01:	49115-49131;
VMYB_02:	42010-42022, 42279-42291, 44651-44663;      and
XFD2_01:	42870-42886, 42910-42926.



10. A composition comprising the nucleic acid molecule of claim 7 and a carrier.

15. A kit comprising the nucleic acid molecule of claim 7.

16. The kit according to claim 15, in which the nucleic acid molecule is labeled with a detectable substance.

17. A solid support comprising the nucleic acid molecule of claim 7.

18. The solid support of claim 17 wherein said support is a microarray.

20. The solid support of claim 18, which further comprises a nucleic acid molecule encoding human mouse double minute 2 homolog, complementary sequence thereof or a portion of said nucleic acid molecule containing at least 20 contiguous nucleotides.

24. An isolated nucleic acid molecule 20-5000 contiguous nucleotides in length consisting of a reverse or forward strand of a contiguous exon-intron region between nucleotides 41738-9502 of SEQ ID NO:4, or contiguous intron-exon region between nucleotides 41738-9502 of SEQ ID NO:4, wherein a sequence segment comprising 41738-9502 of SEQ ID NO:4 encodes human mouse double minute 2 homolog depicted in SEQ ID NO:2.

25. The isolated nucleic acid molecule of claim 24, wherein said nucleic acid molecule is 20-5000 contiguous nucleotides in length and comprises nucleotides 41739-41738, 40645-40646,

36309-36310, 36384-36385, 32994-32995, 33126-33127, 29564-29565, 29615-29616, 25507-25508, 25287-25288, 25383-25384, 25576-25577, 21006-21007, 21168-21169, 13953-13954, 14109-14110, 13188-13189, 13266-13267, 10664-10665 and/or 9504-9503 of SEQ ID NO:4 or their reverse strands.

30. A microarray comprising a plurality of the nucleic acid molecules of claim 7.

31. The microarray of claim 30 wherein said microarray further comprises a nucleic acid molecule encoding human mouse double minute 2 homolog, complementary sequence thereof or a portion of said nucleic acid molecule containing at least 20 contiguous nucleotides.